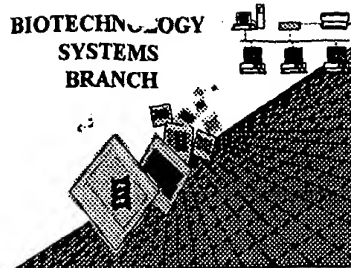


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/844,353
Source: O/PE
Date Processed by STIC: 5/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/844,353

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 J Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/844,353

DATE: 05/11/2001

TIME: 15:18:24

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

Does Not Comply
Corrected Diskette Needed*error throughout*

4 <110> APPLICANT: Ruvkun, Gary
 5 Kimura, Koutarou
 6 Patterson, Garth
 7 Ogg, Scott
 8 Paradis, Suzanne
 9 Tissenbaum, Heidi
 10 Morris, Jason
 11 Koweeek, Allison
 13 <120> TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
 14 IMPAIRED GLUCOSE TOLERANCE CONDITIONS
 17 <130> FILE REFERENCE: 00786/351005
 C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/844,353
 C--> 19 <141> CURRENT FILING DATE: 2001-04-27
 19 <150> PRIOR APPLICATION NUMBER: US 08/857,076
 20 <151> PRIOR FILING DATE: 2000-08-03
 W--> 22 <150> PRIOR APPLICATION NO: US 08/857,076
 23 <151> PRIOR FILING DATE: 1997-05-15
 25 <160> NUMBER OF SEQ ID NOS: 114
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0

*The correct data is
below. Delete these.*

ERRORED SEQUENCES

139 <210> SEQ ID NO: 11
 140 <211> LENGTH: 5816
 141 <212> TYPE: DNA
 142 <213> ORGANISM: Caenorhabditis elegans
 144 <220> FEATURE:
 145 <221> NAME/KEY: misc_feature
 146 <222> LOCATION: (1)...(5816)
 147 <223> OTHER INFORMATION: n = A,T,C or G
 149 <400> SEQUENCE: 11
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 151 ctccccgaaa aaccaacaaa aaacacaaagt ttttgaacac ttgtaaatgc agacagaacg ← 120
 152 atgacgagaa tgaatattgt cagatgtcgg agacgacaca aaattttgga aaatttgga ← 180
 153 gaagagaatc tcggcccgag ctgctcgtcg acgacttcaa caaccgctgc caccgaagct ← 240
 154 ctcggaacaa ccaactgagga tatgaggctt aagcagcagc gaagctcgtc gcgtgccacg ← 300
 155 gagcacgata ttgtcgacgg caatcaccac gacgacgagc acatcacaat gagacggctt ← 360
 156 cgacttgtca aaaattcgcg gacgcggcgt agaacgacgc ccgattcaag tatggactgc ← 420
 157 tatgaggaaa acccgccatc acaaaaactt caataaatta ttcttggtatt tctaaaaagt ← 480
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 161 gcacagtggg ggaagggtcg ctgacaatct catttgtact gaaacacaag acaaaagcac ← 720
 162 aagaagaaat gcactgaagt ctacagccaa gatattccca agacgaattt atcacttttc ← 780
 163 cgcactctacg tgaaattact ggaactctgc tcgtttttga gactgaagga ttagtggatt ← 840
 164 tgcgtaaaaat tttcccaaat cttcgtgtaa ttggaggccg ttcgtgtatt caacactatg ← 900

*Please
move these
total over to
left. They
exceed the
72-character-
per-line limit
(see item 3
on Erra Summary
sheet)*

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/844,353

TIME: 15:18:25

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Output Set: N:\CRF3\05112001\I844353.raw

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180 acatgttccg gaatttacga cgtattgagg caaagtcaat gttcagaaat ctatatgcta 1860
181 tcacagtttt tgaaaatccg aatttaaaaa agctattcga ttcaacgacg gatttgacgc 1920
182 ttgatcgtgg aactgtgtca attgccata acaagatgtt atgcttcaag tatatcaagc 1980
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*move
to
left*

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/844,353

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

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*move
to left*

E--> 244

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please ensure hard returns exist
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247 <211> LENGTH: 1724
248 <212> TYPE: PRT
249 <213> ORGANISM: Caenorhabditis elegans
251 <400> SEQUENCE: 12
252 Met Thr Ser Leu Met Leu Leu Leu Phe Ala Phe Val Gln Pro Cys
253 1 5 10 15
254 Ala Ser Ile Val Glu Lys Arg Cys Gly Pro Ile Asp Ile Arg Asn Arg
255 20 25 30
256 Pro Trp Asp Ile Lys Pro Gln Trp Ser Lys Leu Gly Asp Pro Asn Glu
257 35 40 45
258 Lys Asp Leu Ala Gly Gln Arg Met Val Asn Cys Thr Val Val Glu Gly
259 50 55 60
260 Ser Leu Thr Ile Ser Phe Val Leu Lys His Lys Thr Lys Ala Gln Glu
261 65 70 75 80
262 Glu Met His Arg Ser Leu Gln Pro Arg Tyr Ser Gln Asp Glu Phe Ile
263 85 90 95
264 Thr Phe Pro His Leu Arg Glu Ile Thr Gly Thr Leu Leu Val Phe Glu

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pp 6-8

*Hard returns
need to be
entered after
each cumulative
base total.*

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/844,353

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

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266 Thr Glu Gly Leu Val Asp Leu Arg Lys Ile Phe Pro Asn Leu Arg Val
267          115          120          125
268 Ile Gly Gly Arg Ser Leu Ile Gln His Tyr Ala Leu Ile Ile Tyr Arg
269          130          135          140
270 Asn Pro Asp Leu Glu Ile Gly Leu Asp Lys Leu Ser Val Ile Arg Asn
271 145          150          155          160
272 Gly Gly Val Arg Ile Ile Asp Asn Arg Lys Leu Cys Tyr Thr Lys Thr
273          165          170          175
274 Ile Asp Trp Lys His Leu Ile Thr Ser Ser Ile Asn Asp Val Val Val
275          180          185          190
276 Asp Asn Ala Ala Glu Tyr Ala Val Thr Glu Thr Gly Leu Met Cys Pro
277          195          200          205
278 Arg Gly Ala Cys Glu Glu Asp Lys Gly Glu Ser Lys Cys His Tyr Leu
279          210          215          220
280 Glu Glu Lys Asn Gln Glu Gln Gly Val Glu Arg Val Gln Ser Cys Trp
281 225          230          235          240
282 Ser Asn Thr Thr Cys Gln Lys Ser Cys Ala Tyr Asp Arg Leu Leu Pro
283          245          250          255
284 Thr Lys Glu Ile Gly Pro Gly Cys Asp Ala Asn Gly Asp Arg Cys His
285          260          265          270
286 Asp Gln Cys Val Gly Gly Cys Glu Arg Val Asn Asp Ala Thr Ala Cys
287          275          280          285
288 His Ala Cys Lys Asn Val Tyr His Lys Gly Lys Cys Ile Glu Lys Cys
289          290          295          300
290 Asp Ala His Leu Tyr Leu Leu Leu Gln Arg Arg Cys Val Thr Arg Glu
291 305          310          315          320
292 Gln Cys Leu Gln Leu Asn Pro Val Leu Ser Asn Lys Thr Val Pro Ile
293          325          330          335
294 Lys Ala Thr Ala Gly Leu Cys Ser Asp Lys Cys Pro Asp Gly Tyr Gln
295          340          345          350
296 Ile Asn Pro Asp Asp His Arg Glu Cys Arg Lys Cys Val Gly Lys Cys
297          355          360          365
298 Glu Ile Val Cys Glu Ile Asn His Val Ile Asp Thr Phe Pro Lys Ala
299          370          375          380
300 Gln Ala Ile Arg Leu Cys Asn Ile Ile Asp Gly Asn Leu Thr Ile Glu
301 385          390          395          400
302 Ile Arg Gly Lys Gln Asp Ser Gly Met Ala Ser Glu Leu Lys Asp Ile
303          405          410          415
304 Phe Ala Asn Ile His Thr Ile Thr Gly Tyr Leu Leu Val Arg Gln Ser
305          420          425          430
306 Ser Pro Phe Ile Ser Leu Asn Met Phe Arg Asn Leu Arg Arg Ile Glu
307          435          440          445
308 Ala Lys Ser Leu Phe Arg Asn Leu Tyr Ala Ile Thr Val Phe Glu Asn
309          450          455          460
310 Pro Asn Leu Lys Lys Leu Phe Asp Ser Thr Thr Asp Leu Thr Leu Asp
311 465          470          475          480
312 Arg Gly Thr Val Ser Ile Ala Asn Asn Lys Met Leu Cys Phe Lys Tyr
313          485          490          495

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RAW SEQUENCE LISTING

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Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

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314 Ile Lys Gln Leu Met Ser Lys Leu Asn Ile Pro Leu Asp Pro Ile Asp
315           500           505           510
316 Gln Ser Glu Gly Thr Asn Gly Glu Lys Ala Ile Cys Glu Asp Met Ala
317           515           520           525
318 Ile Asn Val Ser Ile Thr Ala Val Asn Ala Asp Ser Val Phe Phe Ser
319           530           535           540
320 Trp Pro Ser Phe Asn Ile Thr Asp Ile Asp Gln Arg Lys Phe Leu Gly
321 545           550           555           560
322 Tyr Glu Leu Phe Phe Lys Glu Val Pro Arg Ile Asp Glu Asn Met Thr
323           565           570           575
324 Ile Glu Glu Asp Arg Ser Ala Cys Val Asp Ser Trp Gln Ser Val Phe
325           580           585           590
326 Lys Gln Tyr Tyr Glu Thr Ser Asn Gly Glu Pro Thr Pro Asp Ile Phe
327           595           600           605
328 Met Asp Ile Gly Pro Arg Glu Arg Ile Arg Pro Asn Thr Leu Tyr Ala
329           610           615           620
330 Tyr Tyr Val Ala Thr Gln Met Val Leu His Ala Gly Ala Lys Asn Gly
331 625           630           635           640
332 Val Ser Lys Ile Gly Phe Val Arg Thr Ser Tyr Tyr Thr Pro Asp Pro
333           645           650           655
334 Pro Thr Leu Ala Leu Ala Gln Val Asp Ser Asp Ala Ile His Ile Thr
335           660           665           670
336 Trp Glu Ala Pro Leu Gln Pro Asn Gly Asp Leu Thr His Tyr Thr Ile
337           675           680           685
338 Met Trp Arg Glu Asn Glu Val Ser Pro Tyr Glu Glu Ala Glu Lys Phe
339           690           695           700
340 Cys Thr Asp Ala Ser Thr Pro Ala Asn Arg Gln Arg Thr Lys Asp Pro
341 705           710           715           720
342 Lys Glu Thr Ile Val Ala Asp Lys Pro Val Asp Ile Pro Ser Ser Arg
343           725           730           735
344 Thr Val Ala Pro Thr Leu Leu Thr Met Met Gly His Glu Asp Gln Gln
345           740           745           750
346 Lys Thr Cys Ala Ala Thr Pro Gly Cys Cys Ser Cys Ser Ala Ile Glu
347           755           760           765
348 Glu Ser Ser Glu Gln Asn Lys Lys Lys Arg Pro Asp Pro Met Ser Ala
349           770           775           780
350 Ile Glu Ser Ser Ala Phe Glu Asn Lys Leu Leu Asp Glu Val Leu Met
351 785           790           795           800
352 Pro Arg Asp Thr Met Arg Val Arg Arg Ser Ile Glu Asp Ala Asn Arg
353           805           810           815
354 Val Ser Glu Glu Leu Glu Lys Ala Glu Asn Leu Gly Lys Ala Pro Lys
355           820           825           830
356 Thr Leu Gly Gly Lys Lys Pro Leu Ile His Ile Ser Lys Lys Pro
357           835           840           845
358 Ser Ser Ser Ser Thr Thr Ser Thr Pro Ala Pro Thr Ile Ala Ser Met
359           850           855           860
360 Tyr Ala Leu Thr Arg Lys Pro Thr Thr Val Pro Gly Thr Arg Ile Arg
361 865           870           875           880
362 Leu Tyr Glu Ile Tyr Glu Pro Leu Pro Gly Ser Trp Ala Ile Asn Val

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/844,353

DATE: 05/11/2001

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

```

363                               885                               890                               895
364 Ser Ala Leu Ala Leu Asp Asn Ser Tyr Val Ile Arg Asn Leu Lys His
365                               900                               905                               910
366 Tyr Thr Leu Tyr Ala Ile Ser Leu Ser Ala Cys Gln Asn Met Thr Val
367                               915                               920                               925
368 Pro Gly Ala Ser Cys Ser Ile Ser His Arg Ala Gly Ala Leu Lys Arg
369                               930                               935                               940
370 Thr Lys His Ile Thr Asp Ile Asp Lys Val Leu Asn Glu Thr Ile Glu
371 945                               950                               955                               960
372 Trp Arg Phe Met Asn Asn Ser Gln Gln Val Asn Val Thr Trp Asp Pro
373                               965                               970                               975
374 Pro Thr Glu Val Asn Gly Gly Ile Phe Gly Tyr Val Val Lys Leu Lys
375                               980                               985                               990
376 Ser Lys Val Asp Gly Ser Ile Val Met Thr Arg Cys Val Gly Ala Lys
377                               995                               1000                               1005
378 Arg Gly Tyr Ser Thr Arg Asn Gln Gly Val Leu Phe Gln Asn Leu Ala
379 1010                               1015                               1020
380 Asp Gly Arg Tyr Phe Val Ser Val Thr Ala Thr Ser Val His Gly Ala
E--> 381 1025                               1030                               1035                               104
382 Gly Pro Glu Ala Glu Ser Ser Asp Pro Ile Val Val Met Thr Pro Gly
383                               1045                               1050                               1055
384 Phe Phe Thr Val Glu Ile Ile Leu Gly Met Leu Leu Val Phe Leu Ile
385                               1060                               1065                               1070
386 Leu Met Ser Ile Ala Gly Cys Ile Ile Tyr Tyr Tyr Ile Gln Val Arg
387                               1075                               1080                               1085
388 Tyr Gly Lys Lys Val Lys Ala Leu Ser Asp Phe Met Gln Leu Asn Pro
389 1090                               1095                               1100
390 Glu Tyr Cys Val Asp Asn Lys Tyr Asn Ala Asp Asp Trp Glu Leu Arg
E--> 391 1105                               1110                               1115                               112
392 Gln Asp Asp Val Val Leu Gly Gln Gln Cys Gly Glu Gly Ser Phe Gly
393                               1125                               1130                               1135
394 Lys Val Tyr Leu Gly Thr Gly Asn Asn Val Val Ser Leu Met Gly Asp
395                               1140                               1145                               1150
396 Arg Phe Gly Pro Cys Ala Ile Lys Ile Asn Val Asp Asp Pro Ala Ser
397                               1155                               1160                               1165
398 Thr Glu Asn Leu Asn Tyr Leu Met Glu Ala Asn Ile Met Lys Asn Phe
399 1170                               1175                               1180
400 Lys Thr Asn Phe Ile Val Gln Leu Tyr Gly Val Ile Ser Thr Val Glu
E--> 401 1185                               1190                               1195                               120
402 Pro Ala Met Val Val Met Glu Met Met Asp Leu Gly Asn Leu Arg Asp
403                               1205                               1210                               1215
404 Tyr Leu Arg Ser Lys Arg Glu Asp Glu Val Phe Asn Glu Thr Asp Cys
405                               1220                               1225                               1230
406 Asn Phe Phe Asp Ile Ile Pro Arg Asp Lys Phe His Glu Trp Ala Ala
407                               1235                               1240                               1245
408 Gln Ile Cys Asp Gly Met Ala Tyr Leu Glu Ser Leu Lys Phe Cys His
409 1250                               1255                               1260
410 Arg Asp Leu Ala Ala Arg Asn Cys Met Ile Asn Arg Asp Glu Thr Val
E--> 411 1265                               1270                               1275                               128

```

When numbering
last amino acid on
a line, please
end the number
directly below
last letter of
amino acid

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/844,353

DATE: 05/11/2001

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

```

412 Lys Ile Gly Asp Phe Gly Met Ala Arg Asp Leu Phe Tyr His Asp Tyr
413           1285           1290           1295
414 Tyr Lys Pro Ser Gly Lys Arg Met Met Pro Val Arg Trp Met Ser Pro
415           1300           1305           1310
416 Glu Ser Leu Lys Asp Gly Lys Phe Asp Ser Lys Ser Asp Val Trp Ser
417           1315           1320           1325
418 Phe Gly Val Val Leu Tyr Glu Met Val Thr Leu Gly Ala Gln Pro Tyr
419           1330           1335           1340
420 Ile Gly Leu Ser Asn Asp Glu Val Leu Asn Tyr Ile Gly Met Ala Arg
E--> 421 1345           1350           1355           136
422 Lys Val Ile Lys Lys Pro Glu Cys Cys Glu Asn Tyr Trp Tyr Lys Val
423           1365           1370           1375
424 Met Lys Met Cys Trp Arg Tyr Ser Pro Arg Asp Arg Pro Thr Phe Leu
425           1380           1385           1390
426 Gln Leu Val His Leu Leu Ala Ala Glu Ala Ser Pro Glu Phe Arg Asp
427           1395           1400           1405
428 Leu Ser Phe Val Leu Thr Asp Asn Gln Met Ile Leu Asp Asp Ser Glu
429           1410           1415           1420
430 Ala Leu Asp Leu Asp Asp Ile Asp Asp Thr Asp Met Asn Asp Gln Val
E--> 431 1425           1430           1435           144
432 Val Glu Val Ala Pro Asp Val Glu Asn Val Glu Val Gln Ser Asp Ser
433           1445           1450           1455
434 Glu Arg Arg Asn Thr Asp Ser Ile Pro Leu Lys Gln Phe Lys Thr Ile
435           1460           1465           1470
436 Pro Pro Ile Asn Ala Thr Thr Ser His Ser Thr Ile Ser Ile Asp Glu
437           1475           1480           1485
438 Thr Pro Met Lys Ala Lys Gln Arg Glu Gly Ser Leu Asp Glu Glu Tyr
439           1490           1495           1500
440 Ala Leu Met Asn His Ser Gly Gly Pro Ser Asp Ala Glu Val Arg Thr
E--> 441 1505           1510           1515           152
442 Tyr Ala Gly Asp Gly Asp Tyr Val Glu Arg Asp Val Arg Glu Asn Asp
443           1525           1530           1535
444 Val Pro Thr Arg Arg Asn Thr Gly Ala Ser Thr Ser Ser Tyr Thr Gly
445           1540           1545           1550
446 Gly Gly Pro Tyr Cys Leu Thr Asn Arg Gly Gly Ser Asn Glu Arg Gly
447           1555           1560           1565
448 Ala Gly Phe Gly Glu Ala Val Arg Leu Thr Asp Gly Val Gly Ser Gly
449           1570           1575           1580
450 His Leu Asn Asp Asp Asp Tyr Val Glu Lys Glu Ile Ser Ser Met Asp
E--> 451 1585           1590           1595           160
452 Thr Arg Arg Ser Thr Gly Ala Ser Ser Ser Ser Tyr Gly Val Pro Gln
453           1605           1610           1615
454 Thr Asn Trp Ser Gly Asn Arg Gly Ala Thr Tyr Tyr Thr Ser Lys Ala
455           1620           1625           1630
456 Gln Gln Ala Ala Thr Ala Ala Ala Ala Ala Ala Ala Leu Gln Gln
457           1635           1640           1645
458 Gln Gln Asn Gly Gly Arg Gly Asp Arg Leu Thr Gln Leu Pro Gly Thr
459           1650           1655           1660
460 Gly His Leu Gln Ser Thr Arg Gly Gly Gln Asp Gly Asp Tyr Ile Glu

```

same
error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/844,353

DATE: 05/11/2001
TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT
Output Set: N:\CRF3\05112001\I844353.raw

E--> 461 1665 1670 1675 168
462 Thr Glu Pro Lys Asn Tyr Arg Asn Asn Gly Ser Pro Ser Arg Asn Gly
463 1685 1690 1695
E--> 464
Asn Ser Arg Asp Ile Phe Asn Gly Arg Ser Ala Phe Gly Glu Asn Glu 1700 1705

*Please ensure.
hard return spots*

466 <210> SEQ ID NO: 13
467 <211> LENGTH: 139
468 <212> TYPE: PRT
469 <213> ORGANISM: Caenorhabditis elegans
471 <400> SEQUENCE: 13
472 Thr Ser Gly Ser Gly Met Gly Pro Thr Thr Leu His Lys Leu Thr Ile
473 1 5 10 15
474 Gly Gly Gln Ile Arg Leu Thr Gly Arg Val Gly Ser Gly Arg Phe Gly
475 20 25 30
476 Asn Val Ser Arg Gly Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val
477 35 40 45
478 Phe Asn Ala Leu Asp Glu Pro Ala Phe His Lys Glu Thr Glu Ile Phe
479 50 55 60
480 Glu Thr Arg Met Leu Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser
481 65 70 75 80
482 Asp Arg Val Asp Thr Gly Phe Val Thr Glu Leu Trp Leu Val Thr Glu
483 85 90 95
484 Tyr His Pro Ser Gly Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val
485 100 105 110

*Please ensure
amino acid
has. are aligned
properly under
respective amino
acids*

E--> 486
Asn Ile Glu Thr Tyr Tyr Asn Leu Met Arg Ser Thr Ala Ser Gly Leu 115 120

488 <210> SEQ ID NO: 14
489 <211> LENGTH: 62
490 <212> TYPE: PRT
491 <213> ORGANISM: Caenorhabditis elegans
493 <400> SEQUENCE: 14
494 Glu Asp Ala Ala Ser Asp Ile Ile Ala Asn Glu Asn Tyr Lys Cys Gly
495 1 5 10 15
496 Thr Val Arg Tyr Leu Ala Pro Glu Ile Leu Asn Ser Thr Met Gln Phe
497 20 25 30

hard return

hard return

E--> 498
Thr Val Phe Glu Ser Tyr Gln Cys Ala Asp Val Tyr Ser Phe Ser Leu 35 40

500 <210> SEQ ID NO: 15
501 <211> LENGTH: 31
502 <212> TYPE: PRT
503 <213> ORGANISM: Caenorhabditis elegans
505 <400> SEQUENCE: 15

hard return

E--> 506
Lys Pro Ala Met Ala His Arg Asp Ile Lys Ser Lys Asn Ile Met Val 1 5 10

508 <210> SEQ ID NO: 16
509 <211> LENGTH: 72
510 <212> TYPE: PRT
511 <213> ORGANISM: Caenorhabditis elegans
513 <400> SEQUENCE: 16
514 Ile Pro Tyr Ile Glu Trp Thr Asp Arg Asp Pro Gln Asp Ala Gln Met
515 1 5 10 15
516 Phe Asp Val Val Cys Thr Arg Arg Leu Arg Pro Thr Glu Asn Pro Leu
517 20 25 30

next page

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/844,353

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

518 Trp Lys Asp His Pro Glu Met Lys His Ile Met Glu Ile Ile Lys Thr
 519 35 40 45 *hard return*

E--> 520
 Cys Trp Asn Gly Asn Pro Ser Ala Arg Phe Thr Ser Tyr Ile Cys Arg 50 55
 522 <210> SEQ ID NO: 17
 523 <211> LENGTH: 150
 524 <212> TYPE: PRT
 525 <213> ORGANISM: Caenorhabditis elegans
 527 <400> SEQUENCE: 17
 528 Tyr Phe Glu Ser Val Asp Arg Phe Leu Tyr Ser Cys Val Gly Tyr Ser
 529 1 5 10 15
 530 Val Ala Thr Tyr Ile Met Gly Ile Lys Asp Arg His Ser Asp Asn Leu
 531 20 25 30
 532 Met Leu Thr Glu Asp Gly Lys Tyr Val His Ile Asp Phe Gly His Ile
 533 35 40 45
 534 Leu Gly His Gly Lys Thr Lys Leu Gly Ile Gln Arg Asp Arg Gln Pro
 535 50 55 60
 536 Phe Ile Leu Thr Glu His Phe Met Thr Val Ile Arg Ser Gly Lys Ser
 537 65 70 75 80
 538 Val Asp Gly Asn Ser His Glu Leu Gln Lys Phe Lys Thr Leu Cys Val
 539 85 90 95
 540 Glu Ala Tyr Glu Val Met Trp Asn Asn Arg Asp Leu Phe Val Ser Leu
 541 100 105 110
 542 Phe Thr Leu Met Leu Gly Met Glu Leu Pro Glu Leu Ser Thr Lys Ala *same line*

E--> 543
 115 120 125 ✓ Asp Leu Asp His Leu Lys Lys Thr Leu Phe Cy:
 545 <210> SEQ ID NO: 18
 546 <211> LENGTH: 113
 547 <212> TYPE: PRT
 548 <213> ORGANISM: Caenorhabditis elegans
 550 <400> SEQUENCE: 18
 551 Ser Pro Leu Asp Pro Val Tyr Lys Leu Gly Glu Met Ile Ile Asp Lys
 552 1 5 10 15
 553 Ala Ile Val Leu Gly Ser Ala Lys Arg Pro Leu Met Leu His Trp Lys
 554 20 25 30
 555 Asn Lys Asn Pro Lys Ser Asp Leu His Leu Pro Phe Cys Ala Met Ile
 556 35 40 45
 557 Phe Lys Asn Gly Asp Asp Leu Arg Gln Asp Met Leu Val Leu Gln Val
 558 50 55 60
 559 Leu Glu Val Met Asp Asn Ile Trp Lys Ala Ala Asn Ile Asp Cys Cys
 560 65 70 75 80
 561 Leu Asn Pro Tyr Ala Val Leu Pro Met Gly Glu Met Ile Gly Ile Ile

E--> 562
 85 90 95 ✓ Glu Val Val Pro Asn Cys Lys Thr Ile Phe Gl:
 564 <210> SEQ ID NO: 19
 565 <211> LENGTH: 106
 566 <212> TYPE: PRT
 567 <213> ORGANISM: Caenorhabditis elegans
 569 <400> SEQUENCE: 19
 570 Leu Ala Phe Val Trp Thr Asp Arg Glu Asn Phe Ser Glu Leu Tyr Val
 571 1 5 10 15
 572 Met Leu Glu Lys Trp Lys Pro Pro Ser Val Ala Ala Ala Leu Thr Leu

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/844,353

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

```

573          20          25          30
574 Leu Gly Lys Arg Cys Thr Asp Arg Val Ile Arg Lys Phe Ala Val Glu
575          35          40          45
576 Lys Leu Asn Glu Gln Leu Ser Pro Val Thr Phe His Leu Phe Ile Leu
577          50          55          60
578 Pro Leu Ile Gln Ala Leu Lys Tyr Glu Pro Arg Ala Gln Ser Glu Val
579 65          70          75          80

```

E--> 580

Gly Met Met Leu Leu Thr Arg Ala Leu Cys Asp Tyr Arg Ile Gly His

85

90

582 <210> SEQ ID NO: 20

583 <211> LENGTH: 139

584 <212> TYPE: PRT

585 <213> ORGANISM: Caenorhabditis elegans

587 <400> SEQUENCE: 20

588 Glu Tyr Trp Ile Val Thr Glu Phe His Glu Arg Leu Ser Leu Tyr Glu

589 1 5 10 15

590 Leu Leu Lys Asn Asn Val Ile Ser Ile Thr Ser Ala Asn Arg Ile Ile

591 20 25 30

592 Met Ser Met Ile Asp Gly Leu Gln Phe Leu His Asp Asp Arg Pro Tyr

593 35 40 45

594 Phe Phe Gly His Pro Lys Lys Pro Ile Ile His Arg Asp Ile Lys Ser

595 50 55 60

596 Lys Asn Ile Leu Val Lys Ser Asp Met Thr Thr Cys Ile Ala Asp Phe

597 65 70 75 80

598 Gly Leu Ala Arg Ile Tyr Ser Tyr Asp Ile Glu Gln Ser Asp Leu Leu

599 85 90 95

600 Gly Gln Val Gly Thr Lys Arg Tyr Met Ser Pro Glu Met Leu Glu Gly

601 100 105 110

E--> 602

Ala Thr Glu Phe Thr Pro Thr Ala Phe Lys Ala Met Asp Val Tyr Ser

115

120

604 <210> SEQ ID NO: 21

605 <211> LENGTH: 61

606 <212> TYPE: PRT

607 <213> ORGANISM: Caenorhabditis elegans

609 <400> SEQUENCE: 21

610 Ile Gly Phe Asp Pro Thr Ile Gly Arg Met Arg Asn Tyr Val Val Ser

611 1 5 10 15

612 Lys Lys Glu Arg Pro Gln Trp Arg Asp Glu Ile Ile Lys His Glu Tyr

613 20 25 30

E--> 614

Met Ser Leu Leu Lys Lys Val Thr Glu Glu Met Trp Asp Pro Glu Ala

35

40

616 <210> SEQ ID NO: 22

617 <211> LENGTH: 20

618 <212> TYPE: PRT

619 <213> ORGANISM: Caenorhabditis elegans

621 <400> SEQUENCE: 22

E--> 622

Pro Ile Thr Asp Phe Gln Leu Ile Ser Lys Gly Arg Phe Gly Lys Val 1

5

10

624 <210> SEQ ID NO: 23

625 <211> LENGTH: 163

626 <212> TYPE: PRT

627 <213> ORGANISM: Caenorhabditis elegans

629 <400> SEQUENCE: 23

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/844,353

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

```

630 Thr Asp Ser Glu Thr Arg Ser Arg Phe Ser Leu Gly Trp Tyr Asn Asn
631 1 5 10 15
632 Pro Asn Arg Ser Pro Gln Thr Ala Glu Val Arg Gly Leu Ile Gly Lys
633 20 25 30
634 Gly Val Arg Phe Tyr Leu Leu Ala Gly Glu Val Tyr Val Glu Asn Leu
635 35 40 45
636 Cys Asn Ile Pro Val Phe Val Gln Ser Ile Gly Ala Asn Met Lys Asn
637 50 55 60
638 Gly Phe Gln Leu Asn Thr Val Ser Lys Leu Pro Thr Gly Thr Met
639 65 70 75 80
640 Lys Val Phe Asp Met Arg Leu Phe Ser Lys Gln Leu Arg Thr Ala Ala
641 85 90 95
642 Glu Lys Thr Tyr Gln Asp Val Tyr Cys Leu Ser Arg Met Cys Thr Val
643 100 105 110
644 Arg Val Ser Phe Cys Lys Gly Trp Gly Glu His Tyr Arg Arg Ser Thr
645 115 120 125
646 Val Leu Arg Ser Pro Val Trp Phe Gln Ala His Leu Asn Asn Pro Met

```

E--> 647

```

130 135 140 His Trp Val Asp Ser Val Leu Thr Cys Met Gl

```

649 <210> SEQ ID NO: 24

650 <211> LENGTH: 44

651 <212> TYPE: PRT

652 <213> ORGANISM: Caenorhabditis elegans

654 <400> SEQUENCE: 24

655 Arg Ala Phe Arg Phe Pro Val Ile Arg Tyr Glu Ser Gln Val Lys Ser

656 1 5 10 15

E--> 657

```

Ile Leu Thr Cys Arg His Ala Phe Asn Ser His Ser Arg Asn Val Cys 20 25

```

659 <210> SEQ ID NO: 25

660 <211> LENGTH: 38

661 <212> TYPE: PRT

662 <213> ORGANISM: Caenorhabditis elegans

664 <400> SEQUENCE: 25

665 Val Glu Tyr Glu Glu Ser Pro Ser Trp Leu Lys Leu Ile Tyr Tyr Glu

E--> 666

```

1 5 10 15 Glu Gly Thr Met Ile Gly Glu Lys Ala Asp Val

```

668 <210> SEQ ID NO: 26

669 <211> LENGTH: 60

670 <212> TYPE: PRT

671 <213> ORGANISM: Caenorhabditis elegans

673 <400> SEQUENCE: 26

674 Asn Leu Ala Glu Thr Gly His Ser Lys Ile Met Arg Ala Ala His Lys

675 1 5 10 15

676 Val Ser Asn Pro Glu Ile Gly Tyr Cys Cys His Pro Thr Glu Tyr Asp

677 20 25 30

E--> 678

```

Tyr Ile Lys Leu Ile Tyr Val Asn Arg Asp Gly Arg Val Ser Ile Ala 35 40

```

680 <210> SEQ ID NO: 27

681 <211> LENGTH: 20

682 <212> TYPE: PRT

683 <213> ORGANISM: Caenorhabditis elegans

685 <400> SEQUENCE: 27

E--> 686

```

Asp Trp Ile Val Ala Pro Pro Arg Tyr Asn Ala Tyr Met Cys Arg Gly 1 5 10

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/844,353
 DATE: 05/11/2001
 TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT
 Output Set: N:\CRF3\05112001\I844353.raw

688 <210> SEQ ID NO: 28
 689 <211> LENGTH: 43
 690 <212> TYPE: PRT
 691 <213> ORGANISM: Caenorhabditis elegans
 693 <400> SEQUENCE: 28
 694 Val Cys Asn Ala Glu Ala Gln Ser Lys Gly Cys Cys Leu Tyr Asp Leu
 695 1 5 10 15

E--> 696

Glu Ile Glu Phe Glu Lys Ile Gly Trp Asp Trp Ile Val Ala Pro Pro 20 25

698 <210> SEQ ID NO: 29
 699 <211> LENGTH: 70
 700 <212> TYPE: PRT
 701 <213> ORGANISM: Caenorhabditis elegans
 703 <400> SEQUENCE: 29
 704 Asp Cys His Tyr Asn Ala His His Phe Asn Leu Ala Glu Thr Gly His
 705 1 5 10 15
 706 Ser Lys Ile Met Arg Ala Ala His Lys Val Ser Asn Pro Glu Ile Gly
 707 20 25 30
 708 Tyr Cys Cys His Pro Thr Glu Tyr Asp Tyr Ile Lys Leu Ile Tyr Val

E--> 709

35 40 45 Asn Arg Asp Gly Arg Val Ser Ile Ala Asn Val

711 <210> SEQ ID NO: 30
 712 <211> LENGTH: 35
 713 <212> TYPE: PRT
 714 <213> ORGANISM: Caenorhabditis elegans
 716 <400> SEQUENCE: 30
 717 Cys Cys Leu Tyr Asp Leu Glu Ile Glu Phe Glu Lys Ile Gly Trp Asp

E--> 718

1 5 10 15 Trp Ile Val Ala Pro Pro Arg Tyr Asn Ala Ty

770 <210> SEQ ID NO: 34
 771 <211> LENGTH: 131
 772 <212> TYPE: PRT
 773 <213> ORGANISM: Caenorhabditis elegans
 775 <400> SEQUENCE: 34
 776 Asn Thr Thr Cys Gln Lys Ser Cys Ala Tyr Asp Arg Leu Leu Pro Thr
 777 1 5 10 15
 778 Lys Glu Ile Gly Pro Gly Cys Asp Ala Asn Gly Asp Arg Cys His Asp
 779 20 25 30
 780 Gln Cys Val Gly Gly Cys Glu Arg Val Asn Asp Ala Thr Ala Cys His
 781 35 40 45
 782 Ala Cys Lys Asn Val Tyr His Lys Gly Lys Cys Ile Glu Lys Cys Asp
 783 50 55 60
 784 Ala His Leu Tyr Leu Leu Leu Gln Arg Arg Cys Val Thr Arg Glu Gln
 785 65 70 75 80
 786 Cys Leu Gln Leu Asn Pro Val Leu Ser Asn Lys Thr Val Pro Ile Lys
 787 85 90 95
 788 Ala Thr Ala Gly Leu Cys Ser Asp Lys Cys Pro Asp Gly Tyr Gln Ile

E--> 789

100 105 110 Asn Pro Asp Asp His Arg Glu Cys Arg Lys Cy

1551 <210> SEQ ID NO: 48
 1552 <211> LENGTH: 1167
 1553 <212> TYPE: PRT
 1554 <213> ORGANISM: Caenorhabditis elegans

P. 15

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/844,353

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

```

1556 <400> SEQUENCE: 48
1557 Arg Lys Pro Trp Ser Ser Arg Ser Asp Cys Trp Thr Arg Thr Glu Leu
1558 1 5 10 15
1559 Arg Arg Ile Ser Gln Met His Val Asn Ile Leu His Pro Gln Leu Gln
1560 20 25 30
1561 Thr Met Val Glu Gln Trp Gln Met Arg Glu Arg Pro Ser Leu Glu Thr
1562 35 40 45
1563 Glu Asn Gly Lys Gly Ser Leu Leu Leu Glu Asn Glu Gly Val Ala Asp
1564 50 55 60
1565 Ile Ile Thr Met Cys Pro Phe Gly Glu Val Ile Ser Val Val Phe Pro
1566 65 70 75 80
1567 Trp Phe Leu Ala Asn Val Arg Thr Ser Leu Glu Ile Lys Leu Ser Asp
1568 85 90 95
1569 Phe Lys His Gln Leu Phe Glu Leu Ile Ala Pro Met Lys Trp Gly Thr
1570 100 105 110
1571 Tyr Ser Val Lys Pro Gln Asp Tyr Val Phe Arg Gln Leu Asn Asn Phe
1572 115 120 125
1573 Gly Glu Ile Glu Val Ile Phe Asn Asp Asp Gln Pro Leu Ser Lys Leu
1574 130 135 140
1575 Glu Leu His Gly Thr Phe Pro Met Leu Phe Leu Tyr Gln Pro Asp Gly
1576 145 150 155 160
1577 Ile Asn Arg Asp Lys Glu Leu Met Ser Asp Ile Ser His Cys Leu Gly
1578 165 170 175
1579 Tyr Ser Leu Asp Lys Leu Glu Glu Ser Leu Asp Glu Glu Leu Arg Gln
1580 180 185 190
1581 Phe Arg Ala Ser Leu Trp Ala Arg Thr Lys Lys Thr Cys Leu Thr Arg
1582 195 200 205
1583 Gly Leu Glu Gly Thr Ser His Tyr Ala Phe Pro Glu Glu Gln Tyr Leu
1584 210 215 220
1585 Cys Val Gly Glu Ser Cys Pro Lys Asp Leu Glu Ser Lys Val Lys Ala
1586 225 230 235 240
1587 Ala Lys Leu Ser Tyr Gln Met Phe Trp Arg Lys Arg Lys Ala Glu Ile
1588 245 250 255
1589 Asn Gly Val Cys Glu Lys Met Met Lys Ile Gln Ile Glu Phe Asn Pro
1590 260 265 270
1591 Asn Glu Thr Pro Lys Ser Leu Leu His Thr Phe Leu Tyr Glu Met Arg
1592 275 280 285
1593 Lys Leu Asp Val Tyr Asp Thr Asp Asp Pro Ala Asp Glu Gly Trp Phe
1594 290 295 300
1595 Leu Gln Leu Ala Gly Arg Thr Thr Phe Val Thr Asn Pro Asp Val Lys
1596 305 310 315 320
1597 Leu Thr Ser Tyr Asp Gly Val Arg Ser Glu Leu Glu Ser Tyr Arg Cys
1598 325 330 335
1599 Pro Gly Phe Val Val Arg Arg Gln Ser Leu Val Leu Lys Asp Tyr Cys
1600 340 345 350
1601 Arg Pro Lys Pro Leu Tyr Glu Pro His Tyr Val Arg Ala His Glu Arg
1602 355 360 365
1603 Lys Leu Ala Leu Asp Val Leu Ser Val Ser Ile Asp Ser Thr Pro Lys
1604 370 375 380

```

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Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

```

1605 Gln Ser Lys Asn Ser Asp Met Val Met Thr Asp Phe Arg Pro Thr Ala
1606 385                               390                               395                               400
1607 Ser Leu Lys Gln Val Ser Leu Trp Asp Leu Asp Ala Asn Leu Met Ile
1608                               405                               410                               415
1609 Arg Pro Val Asn Ile Ser Gly Phe Asp Phe Pro Ala Asp Val Asp Met
1610                               420                               425                               430
1611 Tyr Val Arg Ile Glu Phe Ser Val Tyr Val Gly Thr Leu Thr Leu Ala
1612                               435                               440                               445
1613 Ser Lys Ser Thr Thr Lys Val Asn Ala Gln Phe Ala Lys Trp Asn Lys
1614                               450                               455                               460
1615 Glu Met Tyr Thr Phe Asp Leu Tyr Met Lys Asp Met Pro Pro Ser Ala
1616 465                               470                               475                               480
1617 Val Leu Ser Ile Arg Val Leu Tyr Gly Lys Val Lys Leu Lys Ser Glu
1618                               485                               490                               495
1619 Glu Phe Glu Val Gly Trp Val Asn Met Ser Leu Thr Asp Trp Arg Asp
1620                               500                               505                               510
1621 Glu Leu Arg Gln Gly Gln Phe Leu Phe His Leu Trp Ala Pro Glu Pro
1622                               515                               520                               525
1623 Thr Ala Asn Arg Ser Arg Ile Gly Glu Asn Gly Ala Arg Ile Gly Thr
1624                               530                               535                               540
1625 Asn Ala Ala Val Thr Ile Glu Ile Ser Ser Tyr Gly Gly Arg Val Arg
1626 545                               550                               555                               560
1627 Met Pro Ser Gln Gly Gln Tyr Thr Tyr Leu Val Lys His Arg Ser Thr
1628                               565                               570                               575
1629 Trp Thr Glu Thr Leu Asn Ile Met Gly Asp Asp Tyr Glu Ser Cys Ile
1630                               580                               585                               590
1631 Arg Asp Pro Gly Tyr Lys Lys Leu Gln Met Leu Val Lys Lys His Glu
1632                               595                               600                               605
1633 Ser Gly Ile Val Leu Glu Glu Asp Glu Gln Arg His Val Trp Met Trp
1634                               610                               615                               620
1635 Arg Arg Tyr Ile Gln Lys Gln Glu Pro Asp Leu Leu Ile Val Leu Ser
1636 625                               630                               635                               640
1637 Glu Leu Ala Phe Val Trp Thr Asp Arg Glu Asn Phe Ser Glu Leu Tyr
1638                               645                               650                               655
1639 Val Met Leu Glu Lys Trp Lys Pro Pro Ser Val Ala Ala Ala Leu Thr
1640                               660                               665                               670
1641 Leu Leu Gly Lys Arg Cys Thr Asp Arg Val Ile Arg Lys Phe Ala Val
1642                               675                               680                               685
1643 Glu Lys Leu Asn Glu Gln Leu Ser Pro Val Thr Phe His Leu Phe Ile
1644                               690                               695                               700
1645 Leu Pro Leu Ile Gln Ala Leu Lys Tyr Glu Pro Arg Ala Gln Ser Glu
1646 705                               710                               715                               720
1647 Val Gly Met Met Leu Leu Thr Arg Ala Leu Cys Asp Tyr Arg Ile Gly
1648                               725                               730                               735
1649 His Arg Leu Phe Trp Leu Leu Arg Ala Glu Ile Ala Arg Leu Arg Asp
1650                               740                               745                               750
1651 Cys Asp Leu Lys Ser Glu Glu Tyr Arg Arg Ile Ser Leu Leu Met Glu
1652                               755                               760                               765
1653 Ala Tyr Leu Arg Gly Asn Glu Glu His Ile Lys Ile Ile Thr Arg Gln

```


RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/844,353

TIME: 15:18:25

Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

```

1654      770      775      780
1655 Val Asp Met Val Asp Glu Leu Thr Arg Ile Ser Thr Leu Val Lys Gly
1656 785      790      795      800
1657 Met Pro Lys Asp Val Ala Thr Met Lys Leu Arg Asp Glu Leu Arg Ser
1658      805      810      815
1659 Ile Ser His Lys Met Glu Asn Met Asp Ser Pro Leu Asp Pro Val Tyr
1660      820      825      830
1661 Lys Leu Gly Glu Met Ile Ile Asp Lys Ala Ile Val Leu Gly Ser Ala
1662      835      840      845
1663 Lys Arg Pro Leu Met Leu His Trp Lys Asn Lys Asn Pro Lys Ser Asp
1664      850      855      860
1665 Leu His Leu Pro Phe Cys Ala Met Ile Phe Lys Asn Gly Asp Asp Leu
1666 865      870      875      880
1667 Arg Gln Asp Met Leu Val Leu Gln Val Leu Glu Val Met Asp Asn Ile
1668      885      890      895
1669 Trp Lys Ala Ala Asn Ile Asp Cys Cys Leu Asn Pro Tyr Ala Val Leu
1670      900      905      910
1671 Pro Met Gly Glu Met Ile Gly Ile Ile Glu Val Val Pro Asn Cys Lys
1672      915      920      925
1673 Thr Ile Phe Glu Ile Gln Val Gly Thr Gly Phe Met Asn Thr Ala Val
1674      930      935      940
1675 Arg Ser Ile Asp Pro Ser Phe Met Asn Lys Trp Ile Arg Lys Gln Cys
1676 945      950      955      960
1677 Gly Ile Glu Asp Glu Lys Lys Lys Ser Lys Lys Asp Ser Thr Lys Asn
1678      965      970      975
1679 Pro Ile Glu Lys Lys Ile Asp Asn Thr Gln Ala Met Lys Lys Tyr Phe
1680      980      985      990
1681 Glu Ser Val Asp Arg Phe Leu Tyr Ser Cys Val Gly Tyr Ser Val Ala
1682      995      1000      1005
1683 Thr Tyr Ile Met Gly Ile Lys Asp Arg His Ser Asp Asn Leu Met Leu
1684      1010      1015      1020
1685 Thr Glu Asp Gly Lys Tyr Val His Ile Asp Phe Gly His Ile Leu Gly
E--> 1686 1025      1030      1035      1040 fix number
1687 His Gly Lys Thr Lys Leu Gly Ile Gln Arg Asp Arg Gln Pro Phe Ile
1688      1045      1050      1055
1689 Leu Thr Glu His Phe Met Thr Val Ile Arg Ser Gly Lys Ser Val Asp
1690      1060      1065      1070
1691 Gly Asn Ser His Glu Leu Gln Lys Phe Lys Thr Leu Cys Val Glu Ala
1692      1075      1080      1085
1693 Tyr Glu Val Met Trp Asn Asn Arg Asp Leu Phe Val Ser Leu Phe Thr
1694      1090      1095      1100
1695 Leu Met Leu Gly Met Glu Leu Pro Glu Leu Ser Thr Lys Ala Asp Leu
E--> 1696 1105      1110      1115      1120 hard return
1697 Asp His Leu Lys Lys Thr Leu Phe Cys Asn Gly Glu Ser Lys Glu Glu
1698      1125      1130      1135
E--> 1699
Ala Arg Lys Phe Phe Ala Gly Ile Tyr Glu Glu Ala Phe Asn Gly Ser      1140      1145
1874 <210> SEQ ID NO: 56
1875 <211> LENGTH: 109
1876 <212> TYPE: PRT

```

RAW SEQUENCE LISTING

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TIME: 15:18:25

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1877 <213> ORGANISM: Caenorhabditis elegans
 1879 <400> SEQUENCE: 56
 1880 Asp Asp Thr Val Ser Gly Lys Lys Thr Thr Thr Arg Arg Asn Ala Trp
 1881 1 5 10 15
 1882 Gly Asn Met Ser Tyr Ala Glu Leu Ile Thr Thr Ala Ile Met Ala Ser
 1883 20 25 30
 1884 Pro Glu Lys Arg Leu Thr Leu Ala Gln Val Tyr Glu Trp Met Val Gln
 1885 35 40 45
 1886 Asn Val Pro Tyr Phe Arg Asp Lys Gly Asp Ser Asn Ser Ser Ala Gly
 1887 50 55 60
 1888 Trp Lys Asn Ser Ile Arg His Asn Leu Ser Leu His Ser Arg Phe Met
 1889 65 70 75 80

E--> 1890

Arg Ile Gln Asn Glu Gly Ala Gly Lys Ser Ser Trp Trp Val Ile Asn

85

90

2114 <210> SEQ ID NO: 70

2115 <211> LENGTH: 29

2116 <212> TYPE: PRT

2117 <213> ORGANISM: Caenorhabditis elegans

2119 <400> SEQUENCE: 70

E--> 2120

Asn Glu Met Leu Asp Pro Glu Pro Lys Tyr Pro Lys Glu Glu Lys Pro 1

5

10

2122 <210> SEQ ID NO: 71

2123 <211> LENGTH: 29

2124 <212> TYPE: PRT

2125 <213> ORGANISM: Caenorhabditis elegans

2127 <400> SEQUENCE: 71

E--> 2128

Gln Leu Gly Lys Ala Phe Glu Ala Lys Val Pro Thr Ile Thr Ile Asp 1

5

10

2281 <210> SEQ ID NO: 83

2282 <211> LENGTH: 46

2283 <212> TYPE: PRT

2284 <213> ORGANISM: Caenorhabditis elegans

2286 <400> SEQUENCE: 83

2287 Glu Ile Gly Leu Asp Lys Leu Ser Val Ile Arg Asn Gly Gly Val Arg

2288 1 5 10 15

E--> 2289

Ile Ile Asp Asn Arg Lys Leu Cys Tyr Thr Lys Thr Ile Asp Trp Lys

20

25

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/844,353

DATE: 05/11/2001

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Input Set : A:\00786.351005.SEQLIST.TXT

Output Set: N:\CRF3\05112001\I844353.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application No
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:288 W: Application Number is Repeated, <150> PRIOR APPLICATION NUMBER
L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:244 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:244 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5816 Found:5640 SEQ:11
L:381 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:464 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1724 Found:1696 SEQ:12
L:486 M:252 E: No. of Seq. differs, <211>LENGTH:Input:139 Found:112 SEQ:13
L:498 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:32 SEQ:14
L:506 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:520 M:252 E: No. of Seq. differs, <211>LENGTH:Input:72 Found:48 SEQ:16
L:543 M:252 E: No. of Seq. differs, <211>LENGTH:Input:150 Found:128 SEQ:17
L:562 M:252 E: No. of Seq. differs, <211>LENGTH:Input:113 Found:96 SEQ:18
L:580 M:252 E: No. of Seq. differs, <211>LENGTH:Input:106 Found:80 SEQ:19
L:602 M:252 E: No. of Seq. differs, <211>LENGTH:Input:139 Found:112 SEQ:20
L:614 M:252 E: No. of Seq. differs, <211>LENGTH:Input:61 Found:32 SEQ:21
L:622 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:0 SEQ:22
L:647 M:252 E: No. of Seq. differs, <211>LENGTH:Input:163 Found:144 SEQ:23
L:657 M:252 E: No. of Seq. differs, <211>LENGTH:Input:44 Found:16 SEQ:24
L:666 M:252 E: No. of Seq. differs, <211>LENGTH:Input:38 Found:16 SEQ:25
L:678 M:252 E: No. of Seq. differs, <211>LENGTH:Input:60 Found:32 SEQ:26
L:686 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:0 SEQ:27
L:696 M:252 E: No. of Seq. differs, <211>LENGTH:Input:43 Found:16 SEQ:28
L:709 M:252 E: No. of Seq. differs, <211>LENGTH:Input:70 Found:48 SEQ:29
L:718 M:252 E: No. of Seq. differs, <211>LENGTH:Input:35 Found:16 SEQ:30
L:733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:789 M:252 E: No. of Seq. differs, <211>LENGTH:Input:131 Found:112 SEQ:34
L:806 M:252 E: No. of Seq. differs, <211>LENGTH:Input:103 Found:80 SEQ:35
L:820 M:252 E: No. of Seq. differs, <211>LENGTH:Input:79 Found:48 SEQ:36
L:838 M:252 E: No. of Seq. differs, <211>LENGTH:Input:106 Found:80 SEQ:37
L:850 M:252 E: No. of Seq. differs, <211>LENGTH:Input:60 Found:32 SEQ:38
L:902 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:902 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2784 Found:2640 SEQ:39
L:1006 M:252 E: No. of Seq. differs, <211>LENGTH:Input:796 Found:768 SEQ:40
L:1118 M:252 E: No. of Seq. differs, <211>LENGTH:Input:858 Found:832 SEQ:41
L:1234 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1234 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1234 M:252 E: No. of Seq. differs, <211>LENGTH:Input:892 Found:891 SEQ:42
L:1298 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:1298 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3499 Found:3360 SEQ:43
L:1349 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:1349 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2704 Found:2580 SEQ:44
L:1549 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:1549 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3504 Found:3360 SEQ:47
L:1686 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:48

VERIFICATION SUMMARY

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TIME: 15:18:26

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M:332 Repeated in SeqNo=48

L:1699 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1788 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:1788 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3017 Found:2880 SEQ:52
L:1845 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:1845 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3119 Found:2940 SEQ:53
L:1862 M:252 E: No. of Seq. differs, <211>LENGTH:Input:103 Found:80 SEQ:54
L:1872 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:55
L:1890 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1976 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1976 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1976 M:252 E: No. of Seq. differs, <211>LENGTH:Input:655 Found:654 SEQ:57
L:1993 M:252 E: No. of Seq. differs, <211>LENGTH:Input:98 Found:80 SEQ:58
L:2001 M:252 E: No. of Seq. differs, <211>LENGTH:Input:7 Found:0 SEQ:59
L:2021 M:252 E: No. of Seq. differs, <211>LENGTH:Input:121 Found:96 SEQ:60
L:2034 M:252 E: No. of Seq. differs, <211>LENGTH:Input:66 Found:48 SEQ:61
L:2044 M:252 E: No. of Seq. differs, <211>LENGTH:Input:45 Found:16 SEQ:62
L:2056 M:252 E: No. of Seq. differs, <211>LENGTH:Input:57 Found:32 SEQ:63
L:2068 M:252 E: No. of Seq. differs, <211>LENGTH:Input:59 Found:32 SEQ:64
L:2077 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:65
L:2085 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:66
L:2093 M:252 E: No. of Seq. differs, <211>LENGTH:Input:26 Found:0 SEQ:67
L:2102 M:252 E: No. of Seq. differs, <211>LENGTH:Input:39 Found:16 SEQ:68
L:2112 M:252 E: No. of Seq. differs, <211>LENGTH:Input:45 Found:16 SEQ:69
L:2120 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:2128 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:2146 M:252 E: No. of Seq. differs, <211>LENGTH:Input:105 Found:80 SEQ:72
L:2162 M:252 E: No. of Seq. differs, <211>LENGTH:Input:89 Found:64 SEQ:73
L:2289 M:333 E: Wrong sequence grouping, Amino acids not in groups!